

ALIGNMENTS

and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thai/>.

Location/Qualifiers

1. .118507

/organism="Arabidopsis thaliana"

/variety="Columbia"

/db_xref="taxon:3702"

/chromosome="5"

complement(1726. .2207)

/gene="F7J8_5"

/number=1

1726. .3687

/gene="F7J8_5"

complement(join(1726. .2207,2629. .2752,2857. .2962,3091. .3556,3633. .3687))

/gene="F7J8_5"

complement(join(1726. .2207,2629. .2752,2857. .2962,3091. .3556,3633. .3687))

/gene="F7J8_5"

/note="strong similarity to serine/threonine-specific protein kinase NAK, Arabidopsis thaliana, EMBL:AL162874"

/codon_start=1

/product="protein kinase-like protein"

/protein_id="CAB99493.1"

/db_xref="GI:9542860"

/translation="MNCNCTRDAAVFTPTPOAQOOLQKKHSRVSLSDPSTPRFNDSTPTISAYQVIFPTLTLELTITKSRPDYITLGGGFGTYKGIIDNLRLGKLSPLPAVVLNKGQAGREWLTEVNFGLQRHPNLVKLIGYCCEDDHLVYEFNLRSKLENHLERSNPTRIHLKMMIALGAAKGLAFNLNAERPVYTRFKTSNILLDSYTLKLSDFGLAKGPODEDFHVSIRVAGTGYAPAEVYMTGLTARSVDYSFGVLLMLTGKRSVDTRPKEEDNLDMAAPKLNDRKLLQIIDPRLENQSVRAAQKACSLAYCCSNPKARPKSDVETLEPLDLOCTGDALIPCATTTAGAAFAAGGVDPYIMHRRFAAVNGPGALCRBPNPVSGGRACACVR"

complement(2208. .2628)

/number=1

complement(2629. .2752)

/gene="F7J8_5"

/number=2

complement(2753. .2856)

/number=2

complement(2857. .2962)

/gene="F7J8_5"

/number=3

complement(2963. .3090)

/number=3

complement(3091. .3556)

/gene="F7J8_5"

/number=4

complement(3557. .3632)

/number=4

complement(3633. .3687)

/gene="F7J8_5"

/number=5

6055. .8420

/gene="F7J8_10"

6055. .8082

/gene="F7J8_10"

/gene="F7J8_10"

/number=1

join(6055. .8082,8214. .8420)

/gene="F7J8_10"

/note="EST FJ4175 marks 5' end of this gene; 5' UTR contains an intron similarly to predicted proteins, Arabidopsis thaliana"

/codon_start=1

/product="putative protein"

/protein_id="CAB69831.1"

/db_xref="GI:6759426"

/translation="MAKREKASGTDNDNRKTKTRSSHRSRKKECVNKSLENDELVYKMSLPLGLQILKEGSEVHOSNVNLVGLWSESIQRMKHGRAGGEISGRSERVYSTATTSTGCVVNPNSANRCKIDDOVHTCSNLGKVAASRDLOYSLPPOARSJLKKOETLRATSGVGNKGVDPKSRPRTSHSNRETTGLSSGNSAGSLFRDKETKRGSEIATQAKERAKACVDELDDCKEITIDGSEAGITSEKQEFNIFLARSKRSTLAGEPQISREVRNLSDDCKNSFGCLRSQIPSSCPLSPDLPKESDPMMLPLGIDLSKRGCKRRKSKTSLTDFDEPDESRKEHPSPSKRFSFSEFRLSRNFSLKDIISGQPLSSSEDTT

2881 aggaagacaagaggttcgaggaagaagaacagtcgttagctgtaggaagcaaatg 2940
|||||
DB 85204 AGGAGAACAGAGGTTGCAGAGGAGAGAACAGAGGTTAGTGTCTGTAGAGCAATG 85263
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QY 2941 aggaaggtatagaagattatagaagaagaagtcgcat 2979
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DB 85264 AGGAGGTATAGAGAGATTATAGCAAGAGAGTCGTCAT 85302
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RESULT 2
AP002483/c AP002483 167405 bp DNA PLN 26-JAN-2001
LOCUS Oryza sativa genomic DNA, chromosome 1, clone: P0019D06.
DEFINITION AP002483
ACCESSION
VERSION
KEYWORDS
SOURCE Oryza sativa (cultivar: Nipponbare) DNA, clone: P0019D06.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
Oryza.
REFERENCE 1 (bases 1 to 167405)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0019D06
JOURNAL Published only in Database (2000) In press
AUTHORS 2 (bases 1 to 167405)
TITLE Sasaki, T., Matsumoto, T. and Yamamoto, K.
JOURNAL Direct Submission
AUTHORS Submitted (07-JUN-2000) Takuji Sasaki, National Institute of
TITLE Agrobiological Resources, Rice Genome Research Program, Kannondai
JOURNAL 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
AUTHORS (E-mail: tsasaki@ab.affrc.go.jp, URL: http://rgrp.dna.affrc.go.jp/
JOURNAL Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT Genes were predicted from the integrated results of the following:
GENSCAN 1.0, BLASTX 2.0, BLASTY 2.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI NonRedundant protein database, nr
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologues of the coding regions were searched against
NCBI NonRedundant protein database using BLASTP 2.0 with the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with EST homology (covering
almost the entire length of partial sequence) is classified as an
'unknown' protein. A gene predicted with a gene prediction program
is classified as a 'hypothetical' protein.
The orientation of the sequence is from T7 to SP6 of the PAC clone.
Detailed information on overlap and assembly quality together with
annotation of this entry is available at
http://rgrp.dna.affrc.go.jp/Genomeseq.html.
FEATURES
source
1. 167405
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
/clone="P0019D06"
7267..7644
/gene="P0019D06.1"
7267..7644
/gene="P0019D06.1"
7267..7644
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PTPEVGRALHOPRALRCRCHETRASLSWTEELKSAATDADKGGEGSGMETSTK
VKNDDEKLAANAASATPRSR"
complement(join(8744..8754,9205..9316,9401..9556,

9860..9958,10073..10147,10266..10334,10501..10699,
11076..11181,11702..12110))
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complement(join(8744..8754,9205..9316,9401..9556,
9860..9958,10073..10147,10266..10334,10501..10699,
11076..11181,11702..12110))
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/note="contains EST AU100943(C60656)"
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/db_xref="GI:10798818"
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YEKDKIDQAIKAFTEYLRAEETRAVLDGIGGGGGSEQAKPRGLRSATVAA
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AVATEVDSPTPSISSDLVSKMGSEKLVANLPMARENPSTIFFEIDSLCGORG
ECNENEASRRITKTELTVOMOGFNDNSNDVLAATNMHVLVDQARRFEDKITYPLP
DKARKDTEFKIHGTPSLTEGDFVSLAYQTEGSGSDIACVADALFOPVRKTPDA
KEFKIADDDTWPSPESQSPGSIQTMQELASGLAAKILLPISKIDDEVLYVRQPT
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join(13646..13747,14696..14806)
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/note="hypothetical protein"
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/db_xref="GI:10798817"
/translation="MMSKPPKRLPDTGDSGQHFEGAIIDNLVQASCEGHLMINTR
IHTSGETIFDRSAELIHNSPSSNRND"
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complement(join(15584..16217,16229..17164))
/gene="P0019D06.4"
/note="probably inactive due to frameshift in CDS
pseudogene, hypothetical protein
similar to Oryza sativa chromosome 1, P0031E09.21"
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/pseudo
join(17888..18090,18725..18854)
/gene="P0019D06.5"
join(17888..18090,18725..18854)
/gene="P0019D06.5"
/note="contains EST AU062706(C30225)
probably inactive due to stop codons in CDS and no
initiation codon
pseudogene, unknown protein
similar to Oryza sativa chromosome 6, P0675A05.11"
/codon_start=1
/pseudo
join(27010..27084,27806..28026,28208..28500,28715..28906,
29454..29585,29936..29969,30347..30393,30536..30614,
30723..30795,30908..30997,31269..31328,31465..31578,
31712..31772,31860..31978,32505..32600,32678..32817)
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join(27010..27084,27806..28026,28208..28500,28715..28906,
29454..29585,29936..29969,30347..30393,30536..30614,
30723..30795,30908..30997,31269..31328,31465..31578,
31712..31772,31860..31978,32505..32600,32678..32817)
/gene="P0019D06.6"
/note="hypothetical protein
similar to Arabidopsis thaliana chromosome 5, F7A7_30"
/codon_start=1
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/db_xref="GI:10798818"
/translation="MEVNSLIGSVTLQFEDYTLKNNHGLKELYQTCRNLSHSETSSKS
IEIEVRRKRPETIRPMTETPGHVGMPLECSYLYLPLVIDYKKNQLVKRWKRYRY
SLLDLDRPSLIGLEIEIPACVSTGNGAVGSPFHSHALAPHRSSICSPQPPPP
TRASMAELDEEDRGVAPASRRPRHVEEETASPRKMGCIKELIKRYTLIDNS
KLOIHQKNEHMANITLBEKKEKANSIPRAIDETVLPACFPQSVDDTLEIYLMQRP
KTNVIGICHTLVSTLTKYVNLNKLTKGSAASAALRWKSKDIGAEGRLILQDP
FGVLFDDDKPKRMVADPFGSAGSIFELTLPDGVGLTSLASGNLAKAVNGRFPDS
FVLIQNHFFESGNIGVAAKEEYVGAQLGISIVFIMDTSGIKSSVPTLALTWLG